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Complete Genome Sequences of *Krokinobacter* sp. Strain 4H-3-7-5 and *Lacinutrix* sp. Strain 5H-3-7-4, Polysaccharide-Degrading Members of the Family *Flavobacteriaceae*

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Genome Announcement

Complete Genome Sequences of *Krokinobacter* sp. 4H-3-7-5 and *Lacinutrix* sp. 5H-3-7-4, polysaccharide-degrading members of the family *Flavobacteriaceae*

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Abstract

Two members of the family *Flavobacteriaceae* were isolated from subseafloor sediments using artificial seawater with cellulose, xylan and chitin as sole carbon and energy sources. Here, we present the complete genome sequences of *Krokinobacter* sp. 4H-3-7-5 and *Lacinutrix* sp. 5H-3-7-4 which both encode for putatively novel enzymes involved in cellulose, hemicellulose and chitin metabolism.

Members of the family *Flavobacteriaceae* are well-known for degrading complex polymeric substrates in marine habitats (4). Two marine representatives of

25 this family, *Krokinobacter* sp. 4H-3-7-5 and *Lacinutrix* sp. 5H-3-7-4, were isolated
26 from subseafloor sediments at Suruga Bay (Japan) from a depth of 31.4 and 41 m
27 using a mixture of cellulose, xylan and chitin as sole carbon sources in enrichment
28 cultures.

29 To gain insight into the gene repertoire of these organisms the complete
30 genomes of *Krokinobacter* sp. 4H-3-7-5 and of *Lacinutrix* sp. 5H-3-7-4 were
31 generated at the DOE Joint genome Institute (JGI) using Illumina (1) and 454
32 technologies (3). For *Krokinobacter* sp. 4H-3-7-5 we sequenced an Illumina GAii
33 shotgun library which generated 38,286,828 reads (2909 Mb), a 454 Titanium
34 standard library which generated 205,742 reads and a paired end 454 library
35 (average insert size: 11.1 +/- 2.8 kb) which generated 287,950 reads totaling 136.6
36 Mb of 454 data. For *Lacinutrix* sp. 5H-3-7-4 we sequenced an Illumina GAii shotgun
37 library which generated 54,815,066 reads (4,165.9 Mb), a 454 Titanium standard
38 library which generated 268,763 reads and one paired end 454 library with an
39 average insert size of 17 kb which generated 220,650 reads totaling 152.2 Mb of 454
40 data. All general aspects of library construction and sequencing can be found at
41 <http://www.jgi.doe.gov/>. The 454 Titanium standard data and the 454 paired end data
42 were assembled together with Newbler, version 2.3 while the Illumina sequencing
43 data was assembled with VELVET, versions 0.7.63 and 1.0.13 (5).

44 For finishing, Newbler and Illumina VELVET consensus data as well as read
45 pairs in the 454 paired end library were integrated using parallel phrap, versions SPS
46 - 4.24 and 1.080812 (High Performance Software, LLC). Consensus quality was
47 increased by using the software Polisher (Alla Lapidus, unpublished) and possible
48 mis-assemblies were corrected using gapResolution (Cliff Han, unpublished),
49 Dupfinisher (2), or sequencing cloned bridging PCR fragments. Gaps between
50 contigs were closed by editing in Consed, by PCR and by Bubble PCR (J-F Cheng,

unpublished) primer walks. The total size of the *Krokinobacter* sp. 4H-3-7-5 final genome assembly is 3,389,992 bp based on 99.7 Mb of 454 draft data (30x coverage) and 1362 Mb of Illumina draft data (401x coverage). The total size of the final *Lacinutrix* sp. 5H-3-7-4 genome assembly is 3,296,168 bp, based on 124.9 Mb of 454 draft data (37.9x coverage) and 4,072.6 Mb of Illumina draft data (1,234.1x coverage).

The data provides the first publically available genomes for the members of the genera *Krokinobacter* and *Lacinutrix*. 2978 and 2967 putative protein-encoding ORFs could be identified. Both isolates have low G+C contents of 37.2 (*Krokinobacter* sp. 4H-3-7-5) and 30.8% (*Lacinutrix* sp. 5H-3-7-4), respectively. Genome analysis revealed several ORFs for carbohydrate-active enzymes belonging to various glycoside hydrolase families. Further studies will provide significant information to assess the role of both organisms in polysaccharide hydrolysis in marine habitats.

Nucleotide sequence accession number. The complete genome sequences of *Krokinobacter* sp. 4H-3-7-5 and *Lacinutrix* sp. 5H-3-7-4 have been deposited in GenBank under accession numbers CP002528 and CP002825.

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